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RAW SEQUENCE LISTING

DATE: 10/01/2002

PATENT APPLICATION: US/08/875,849C

TIME: 15:07:36

Input Set : A:\LKS944A2.txt

Output Set: N:\CRF4\10012002\H875849C.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION.

6 (i) APPLICANT: Briskin, Michael J.

7 Ringler, Douglas J.

8 Picarella, Dominic

9 Newman, Walter

11 (ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses

12 Thereof

14 (iii) NUMBER OF SEQUENCES: 17

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

18 (B) STREET: 530 Virginia Road, PO Box 9133

19 (C) CITY: Concord

20 (D) STATE: Massachusetts

21 (E) COUNTRY: U.S.A.

22 (F) ZIP: 01742-9133

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/08/875,849C

C--> 32 (B) FILING DATE: 08-Sep-1997

33 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: PCT/US96/02153

37 (B) FILING DATE: 12-FEB-1996

40 (A) APPLICATION NUMBER: US 08/523,004

41 (B) FILING DATE: 01-SEP-1995

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Brook, David E.

45 (B) REGISTRATION NUMBER: 22,592

46 (C) REFERENCE/DOCKET NUMBER: LKS94-04A2

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: 978-341-0036

50 (B) TELEFAX: 978-341-0136

60 (2) INFORMATION FOR SEQ ID NO: 1:

62 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 1624 base pairs

64 (B) TYPE: nucleic acid

65 (C) STRANDEDNESS: double

66 (D) TOPOLOGY: linear

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68      (ii) MOLECULE TYPE: cDNA
70      (ix) FEATURE
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 1..1218
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77 ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTI CTG GGG CTC CTC      48
78 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu
79 1 5 10 15
81 CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG      96
82 Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
83 20 25 30
85 CCG GTG GTG GCC GTG GGC TTG GGC GGC TCG CGC CAG CTC ACC TGC CGC      144
86 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
87 35 40 45
89 CTG GCC TGC GCG GAC CGC GGG GGC TCG GTG CAG TGG CGG GGC CTG GAC      192
90 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
91 50 55 60
93 ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC      240
94 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
95 65 70 75 80
97 GTG CGC AAC GCC TCG CTG TCG GCG GGC GGG ACC CGC GTG TGC GTG GGC      288
98 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
99 85 90 95
101 TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CIT GTG TAC      336
102 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
103 100 105 110
105 GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT      384
106 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
107 115 120 125
109 GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC      432
110 Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
111 130 135 140
113 AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG      480
114 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
115 145 150 155 160
119 GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC CAG      528
120 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
121 165 170 175
123 GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CCG CTG CCG      576
124 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
125 180 185 190
127 CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ACG ATG      624
128 Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
129 195 200 205
131 AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC ATC CCC GTC CTG      672
132 Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
133 210 215 220
135 CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT      720
136 His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro

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137 225                230                235                240
139 CCC AAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CCG GAG TCT      768
140 Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
141                245                250                255
143 CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT      816
144 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
145                260                265                270
147 CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT      864
148 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
149                275                280                285
151 CCC GAC AAG ACC TCC CCG GAG CCC GGC CCC CAG CAG GGC TCC ACA CAC      912
152 Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
153                290                295                300
155 ACC CCC AGG AGC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC      960
156 Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser
157 305                310                315                320
159 CAG GCT GGG CCC ACG CAG GGA GAA GIG ATC CCA ACA GGC TCG TCC AAA      1008
160 Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys
161                325                330                335
163 CCI GCG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG      1056
164 Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
165                340                345                350
167 CTG GGA CIG CTG CTC CTG GCC TIG CCC ACG IAT CAC CTC TGG AAA CGC      1104
168 Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
169                355                360                365
171 TGC CGG CAC CTG GCT GAG GAC GAC ACC CAC CCA CCA GCT TCT CTG AGG      1152
172 Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
173                370                375                380
175 CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA AGG GGG ACC GGC CAG      1200
176 Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
177 385                390                395                400
179 GTC GGG ATC AGC CCC TCC TGAGTGGCCA GCCTTTCCCC CTGTGAAAAGC      1248
180 Val Gly Ile Ser Pro Ser
181                405
184 AAAATAGCTT GGACCCCTTC AAGTIGAGAA CTGGTCAGGG CAAACCTGCC TCCCATTCTA      1308
186 CTCAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCCT CTTTGGAGAA      1368
188 GCICATCAGA AACTCAAAAAG AAGGCCACTG TTTGTCTCAC CTACCCATGA CCTGAAGCCC      1428
190 CTCCCTGAGT GGTCCCCACC TTTCIGGACG GAACCACGTA CTTTTTACAT ACATTGATTC      1488
192 ATGTCTCACC TCTCCCTAAA AATGCGTAAG ACCAAGCTGT GCCCTGACCA CCCTGGGCCC      1548
194 CTGTCTCAGC GACCTCCTGA GGCTTTGGCA AATAAACCTC CTAAAATGAT AAAAAAAAAA      1608
196 AAAAAAAAAA AAAAAA      1624
199 (2) INFORMATION FOR SEQ ID NO: 2:
201      (i) SEQUENCE CHARACTERISTICS:
202          (A) LENGTH: 406 amino acids
203          (B) TYPE: amino acid
204          (D) TOPOLOGY: linear
206      (ii) MOLECULE TYPE: protein
209      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
211 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu

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212	1	5	10	15
214	Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu			
215	20	25	30	
217	Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg			
218	35	40	45	
220	Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp			
221	50	55	60	
223	Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr			
224	65	70	75	80
226	Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly			
227	85	90	95	
229	Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr			
230	100	105	110	
232	Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly			
233	115	120	125	
235	Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro			
236	130	135	140	
238	Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly			
239	145	150	155	160
241	Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Glu Pro Gln			
242	165	170	175	
244	Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro			
245	180	185	190	
247	Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met			
248	195	200	205	
250	Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu			
251	210	215	220	
253	His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro			
254	225	230	235	240
256	Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser			
257	245	250	255	
259	Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro			
260	260	265	270	
262	Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro			
263	275	280	285	
265	Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His			
266	290	295	300	
268	Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser			
269	305	310	315	320
271	Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys			
272	325	330	335	
274	Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val			
275	340	345	350	
277	Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg			
278	355	360	365	
280	Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg			
281	370	375	380	
283	Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln			
284	385	390	395	400

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286 Val Gly Ile Ser Pro Ser
287 405
290 (2) INFORMATION FOR SEQ ID NO: 3:
292 (i) SEQUENCE CHARACTERISTICS:
293 (A) LENGTH: 1539 base pairs
294 (B) TYPE: nucleic acid
295 (C) STRANDEDNESS: Double
296 (D) TOPOLOGY: linear
298 (ii) MOLECULE TYPE: cDNA
300 (ix) FEATURE:
301 (A) NAME/KEY: CDS
302 (B) LOCATION: 1..1146
306 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
308 ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC 48
309 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu
310 1 5 10 15
312 CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG 96
313 Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
314 20 25 30
316 CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC 144
317 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
318 35 40 45
320 CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC 192
321 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
322 50 55 60
324 ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC 240
325 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
326 65 70 75 80
328 GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC 288
329 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
330 85 90 95
332 TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC 336
333 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
334 100 105 110
336 GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT 384
337 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
338 115 120 125
340 GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC 432
341 Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
342 130 135 140
344 AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG 480
345 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
346 145 150 155 160
348 GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG GAG CCC CAG 528
349 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Glu Pro Gln
350 165 170 175
352 GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CCG 576
353 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
354 180 185 190

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